SEQUENCE LISTING

<110> Goossens, Alain
Inze, Dirk

<120> THE USE OF GENES ENCODING MEMBRANE TRANSPORTER PUMPS TO STIMULATE THE PRODUCTION OF SECONDARY METABOLITES IN BIOLOGICAL CELLS

<130> DI/ABC/V082

<150> EP01201407.2
<151> 2001-04-18

<160> 15

<170> PatentIn version 3.1

<210> 1
<211> 4571
<212> DNA
<213> Hyoscyamus muticus

<220>
<221> CDS
<222> (133)..(4407)
<223> n is defined as any nucleotide

<400> 1
atataactaa cttcaccttc tattcattca ttatcaacaa aataatccat tttttatcaa 60

aacttgaagg tgttgttaca agacacaact aatattaatt gctgcatttt aatttaatct 120

tgttgttcca ac atg gag cca tca gat tta agt aat ttc cga ggt cga agt 171
Met Glu Pro Ser Asp Leu Ser Asn Phe Arg Gly Arg Ser
1 5 10

atg aga gga agt atg aga gga agt gta agg gaa aat agt aac tca ata 219
Met Arg Gly Ser Met Arg Gly Ser Val Arg Glu Asn Ser Asn Ser Ile
15 20 25

tgg agg aac aat gga gtt gaa ata ttt tca aga tca act aga gat gaa 267
Trp Arg Asn Asn Gly Val Glu Ile Phe Ser Arg Ser Thr Arg Asp Glu
30 35 40 45

gat gat gaa gag gca tta aaa tgg gca gca ctt gag aaa tta cca aca 315
Asp Asp Glu Glu Ala Leu Lys Trp Ala Ala Leu Glu Lys Leu Pro Thr
50 55 60

tat gat aga tta aga aaa ggt ata ttg ttt gga tca caa ggt act ggt 363
Tyr Asp Arg Leu Arg Lys Gly Ile Leu Phe Gly Ser Gln Gly Thr Gly
65 70 75

gtt gct gaa gtt gat gta gat gat ctt ggt gtt caa caa agg aag aat 411
Val Ala Glu Val Asp Val Asp Asp Leu Gly Val Gln Gln Arg Lys Asn
80 85 90

```
ttg ctt gac aga ctt gtt aaa att gct gaa gaa gat aat gag aag ttc      459
Leu Leu Asp Arg Leu Val Lys Ile Ala Glu Glu Asp Asn Glu Lys Phe
    95                  100                 105

ttg ttg aaa ctc aag aac agg att gac agg gtt ggg att gat ttt cca      507
Leu Leu Lys Leu Lys Asn Arg Ile Asp Arg Val Gly Ile Asp Phe Pro
110                 115                 120                 125

tct ata gaa gtg aga ttt gag cat ctg aat att gag gca gat gca tat      555
Ser Ile Glu Val Arg Phe Glu His Leu Asn Ile Glu Ala Asp Ala Tyr
                130                 135                 140

gtt ggt agc aga gct ttg cct aca ttt acc aac ttc att tct aac ttc      603
Val Gly Ser Arg Ala Leu Pro Thr Phe Thr Asn Phe Ile Ser Asn Phe
            145                 150                 155

att gag tcc ctg ctg gat tca ctt cac atc ctt cca tcg aaa aaa cgt      651
Ile Glu Ser Leu Leu Asp Ser Leu His Ile Leu Pro Ser Lys Lys Arg
        160                 165                 170

tca gtt aca att ctc aag gat gtt agt ggt atc gtc aag ccc tgt cga      699
Ser Val Thr Ile Leu Lys Asp Val Ser Gly Ile Val Lys Pro Cys Arg
    175                 180                 185

atg act ctg ctt tta gga cct cca ggt tct ggg aaa aca act ttg tta      747
Met Thr Leu Leu Leu Gly Pro Pro Gly Ser Gly Lys Thr Thr Leu Leu
190                 195                 200                 205

ctt gct ttg gct gga aaa ctt gat tct gct cta agg gtt acg ggg aag      795
Leu Ala Leu Ala Gly Lys Leu Asp Ser Ala Leu Arg Val Thr Gly Lys
                210                 215                 220

gtg acg tat aat gga cac gaa tta cat gaa ttt gtg cca caa aga act      843
Val Thr Tyr Asn Gly His Glu Leu His Glu Phe Val Pro Gln Arg Thr
            225                 230                 235

gcg gcc tat att agc cag cat gat ttg cat att gga gaa atg act gtc      891
Ala Ala Tyr Ile Ser Gln His Asp Leu His Ile Gly Glu Met Thr Val
        240                 245                 250

aga gaa act ttg gag ttc tct gca aga tgc caa gga gtt ggt tct cgt      939
Arg Glu Thr Leu Glu Phe Ser Ala Arg Cys Gln Gly Val Gly Ser Arg
    255                 260                 265

tac gaa atg ttg gcc gaa ctg tca aga aga gag aaa gcg gct aat atc      987
Tyr Glu Met Leu Ala Glu Leu Ser Arg Arg Glu Lys Ala Ala Asn Ile
270                 275                 280                 285

aaa cca gat gct gat att gac atg ttc atg aag gct gca tca act gaa     1035
Lys Pro Asp Ala Asp Ile Asp Met Phe Met Lys Ala Ala Ser Thr Glu
                290                 295                 300

ggg caa gaa gcc aaa gtg att act gat tat gtt ctt aag att ctg gga     1083
Gly Gln Glu Ala Lys Val Ile Thr Asp Tyr Val Leu Lys Ile Leu Gly
            305                 310                 315
```

```
ctg gat att tgt gca gat act atg gtg gga gat caa atg ata agg ggt     1131
Leu Asp Ile Cys Ala Asp Thr Met Val Gly Asp Gln Met Ile Arg Gly
        320                 325                 330

att tca gga gga cag aag aag cgt gtc act act ggt gaa atg att gtc     1179
Ile Ser Gly Gly Gln Lys Lys Arg Val Thr Thr Gly Glu Met Ile Val
    335                 340                 345

gga ccg tct aaa gcc ctt ttc atg gat gaa att tca act gga ctt gac     1227
Gly Pro Ser Lys Ala Leu Phe Met Asp Glu Ile Ser Thr Gly Leu Asp
350                 355                 360                 365

agt tcc aca act tac tcc atc gtg aat tcc cta aag caa tct gtt caa     1275
Ser Ser Thr Thr Tyr Ser Ile Val Asn Ser Leu Lys Gln Ser Val Gln
                370                 375                 380

atc ttg aaa gga aca gct ctg att tct ctc ttg cag cct gcc ccc gag     1323
Ile Leu Lys Gly Thr Ala Leu Ile Ser Leu Leu Gln Pro Ala Pro Glu
            385                 390                 395

act tac aac ttg ttc gat gat att gtt ctg cta tca gat ggc tac att     1371
Thr Tyr Asn Leu Phe Asp Asp Ile Val Leu Leu Ser Asp Gly Tyr Ile
        400                 405                 410

gtt tat cag ggt cca cga gag gaa gtg ctc gat ttc ttt gaa tcc atg     1419
Val Tyr Gln Gly Pro Arg Glu Glu Val Leu Asp Phe Phe Glu Ser Met
    415                 420                 425

gga ttc aaa tgc ccc aac aga aaa ggc gtg gct gac ttc ttg caa gaa     1467
Gly Phe Lys Cys Pro Asn Arg Lys Gly Val Ala Asp Phe Leu Gln Glu
430                 435                 440                 445

gtt aca tct aag aag gat caa cag caa tat tgg gta aag agg gac gag     1515
Val Thr Ser Lys Lys Asp Gln Gln Gln Tyr Trp Val Lys Arg Asp Glu
                450                 455                 460

cct tat agg ttt att aca tca aaa gaa ttt gct gag gct tat caa tct     1563
Pro Tyr Arg Phe Ile Thr Ser Lys Glu Phe Ala Glu Ala Tyr Gln Ser
            465                 470                 475

ttc cat gtt ggg aga aaa gta agc gat gaa ctt aca acc gca ttt gac     1611
Phe His Val Gly Arg Lys Val Ser Asp Glu Leu Thr Thr Ala Phe Asp
        480                 485                 490

aag agc aaa agc cac cct gct gct ttg act act gaa aag tat ggt att     1659
Lys Ser Lys Ser His Pro Ala Ala Leu Thr Thr Glu Lys Tyr Gly Ile
    495                 500                 505

gga gtg aaa caa ctt ttg aag gtt tgc acg gaa aga gag ttc ctt cta     1707
Gly Val Lys Gln Leu Leu Lys Val Cys Thr Glu Arg Glu Phe Leu Leu
510                 515                 520                 525

atg cag agg aat tca ttt gtt tac atc ttc aaa ttc ttt cag ctt atg     1755
Met Gln Arg Asn Ser Phe Val Tyr Ile Phe Lys Phe Phe Gln Leu Met
                530                 535                 540
```

```
gta att gca ctt atg aca atg acc ata ttt ttt cga act aag atg tct     1803
Val Ile Ala Leu Met Thr Met Thr Ile Phe Phe Arg Thr Lys Met Ser
            545                 550                 555

cgg gat act gag acc gat gga gga att tat tct ggt gct ctc ttt ttt     1851
Arg Asp Thr Glu Thr Asp Gly Gly Ile Tyr Ser Gly Ala Leu Phe Phe
        560                 565                 570

acg gtt gtt atg ctt atg ttt aat ggt ttg tct gag ctt cct ttg aca     1899
Thr Val Val Met Leu Met Phe Asn Gly Leu Ser Glu Leu Pro Leu Thr
    575                 580                 585

ctc tac aag ctc ccg gtc ttc tac aag caa agg gac ttt ctc ttc tat     1947
Leu Tyr Lys Leu Pro Val Phe Tyr Lys Gln Arg Asp Phe Leu Phe Tyr
590                 595                 600                 605

cct tca tgg gct tat gca gtt cct tca tgg atc cta aaa atc cct gta     1995
Pro Ser Trp Ala Tyr Ala Val Pro Ser Trp Ile Leu Lys Ile Pro Val
                610                 615                 620

act ttt ctt gaa gtt ggg atg tgg gtg ttt ctc acc tat tat gtc atc     2043
Thr Phe Leu Glu Val Gly Met Trp Val Phe Leu Thr Tyr Tyr Val Ile
            625                 630                 635

gga ttt gat cct aat gtt gga aga ttt ttc aaa caa ttt ttg cta ctc     2091
Gly Phe Asp Pro Asn Val Gly Arg Phe Phe Lys Gln Phe Leu Leu Leu
        640                 645                 650

ata gta gta aac cag atg gca tca gga ttg ttc agg ttt att gca gca     2139
Ile Val Val Asn Gln Met Ala Ser Gly Leu Phe Arg Phe Ile Ala Ala
    655                 660                 665

gtt gga agg acc atg gga gtt gct agc aca ttt gga gca ttt gcg ctg     2187
Val Gly Arg Thr Met Gly Val Ala Ser Thr Phe Gly Ala Phe Ala Leu
670                 675                 680                 685

ctt tta caa ttt gca ttg ggc ggt ttt gtc ctt gca cga act gac gtg     2235
Leu Leu Gln Phe Ala Leu Gly Gly Phe Val Leu Ala Arg Thr Asp Val
                690                 695                 700

aag gac tgg tgg att tgg gga tac tgg acc tca cca ctt atg ttc tca     2283
Lys Asp Trp Trp Ile Trp Gly Tyr Trp Thr Ser Pro Leu Met Phe Ser
            705                 710                 715

gtg aat gca atc ctt gtg aat gaa ttt gac gga aaa aag tgg aaa cat     2331
Val Asn Ala Ile Leu Val Asn Glu Phe Asp Gly Lys Lys Trp Lys His
        720                 725                 730

att gcg cca aat gga act gag ccg ctt gga cct gca gtg gta aga tct     2379
Ile Ala Pro Asn Gly Thr Glu Pro Leu Gly Pro Ala Val Val Arg Ser
    735                 740                 745

caa ggg ttc ttt ccc gat gca tat tgg tac tgg ata ggt gta ggt gca     2427
Gln Gly Phe Phe Pro Asp Ala Tyr Trp Tyr Trp Ile Gly Val Gly Ala
750                 755                 760                 765
```

```
ctt gtt gga ttc aca gtt ctg ttt aac ata gcc tac agt ctt gct ctc     2475
Leu Val Gly Phe Thr Val Leu Phe Asn Ile Ala Tyr Ser Leu Ala Leu
                770                 775                 780

gct tat ctt aac cca ttc gga aag cca caa gct aca att tca gaa gaa     2523
Ala Tyr Leu Asn Pro Phe Gly Lys Pro Gln Ala Thr Ile Ser Glu Glu
            785                 790                 795

agt gag agc aac gaa aat agt gaa tta tca acc cca ata gct agt aca     2571
Ser Glu Ser Asn Glu Asn Ser Glu Leu Ser Thr Pro Ile Ala Ser Thr
        800                 805                 810

acg gaa gga gat tct gtc ggt gag aat cag aat aag aaa gga atg gtt     2619
Thr Glu Gly Asp Ser Val Gly Glu Asn Gln Asn Lys Lys Gly Met Val
    815                 820                 825

ctt cca ttt gaa ccc cat tcc atc acc ttt gat gaa gtt gta tac tca     2667
Leu Pro Phe Glu Pro His Ser Ile Thr Phe Asp Glu Val Val Tyr Ser
830                 835                 840                 845

gtt gac atg cct ccg gaa atg aga gag caa ggt acc agt gac aat aga     2715
Val Asp Met Pro Pro Glu Met Arg Glu Gln Gly Thr Ser Asp Asn Arg
                850                 855                 860

ttg gta ctt ttg aag agt gtg agt gga gct ttc agg cca ggt gtt ctc     2763
Leu Val Leu Leu Lys Ser Val Ser Gly Ala Phe Arg Pro Gly Val Leu
            865                 870                 875

aca gct ctg atg gga gtt agt gga gcc ggt aaa aca aca ttg atg gat     2811
Thr Ala Leu Met Gly Val Ser Gly Ala Gly Lys Thr Thr Leu Met Asp
        880                 885                 890

gtc tta gct gga agg aaa act gga ggt tac att gac gga agc att aac     2859
Val Leu Ala Gly Arg Lys Thr Gly Gly Tyr Ile Asp Gly Ser Ile Asn
    895                 900                 905

att tct gga tat ccc aag aag caa gaa aca ttt gca cgt att tct gga     2907
Ile Ser Gly Tyr Pro Lys Lys Gln Glu Thr Phe Ala Arg Ile Ser Gly
910                 915                 920                 925

tac tgt gaa caa aac gac atc cat tca cct tat gta aca gtt tat gag     2955
Tyr Cys Glu Gln Asn Asp Ile His Ser Pro Tyr Val Thr Val Tyr Glu
                930                 935                 940

tcc ttg gtt tac tcg gct tgg ctg cgt tta cct caa gac gtt gat gag     3003
Ser Leu Val Tyr Ser Ala Trp Leu Arg Leu Pro Gln Asp Val Asp Glu
            945                 950                 955

aaa aag cga atg atg ttc gtt gaa caa gtt atg gaa ctt gtg gag ctt     3051
Lys Lys Arg Met Met Phe Val Glu Gln Val Met Glu Leu Val Glu Leu
        960                 965                 970

aca cca cta aga tct gcc tta gtc ggg ttg cca gga gtt aat ggt ctg     3099
Thr Pro Leu Arg Ser Ala Leu Val Gly Leu Pro Gly Val Asn Gly Leu
    975                 980                 985
```

```
acg att gca gtt gaa cta gta gca aac ccc tct  atc att ttt atg gac    3147
Thr Ile Ala Val Glu Leu Val Ala Asn Pro Ser  Ile Ile Phe Met Asp
990                 995                 1000                1005

gaa cca act tca gga  ttg gat gca aga gct  gct gca att gtg atg       3192
Glu Pro Thr Ser Gly  Leu Asp Ala Arg Ala  Ala Ala Ile Val Met
                1010                1015                1020

aga gct gtt agg aac  act gtc gat aca ggg  aga act gtt gtt tgt       3237
Arg Ala Val Arg Asn  Thr Val Asp Thr Gly  Arg Thr Val Val Cys
                1025                1030                1035

acc att cat cag cct  agc att gac att ttt  gag gcg ttc gat gag       3282
Thr Ile His Gln Pro  Ser Ile Asp Ile Phe  Glu Ala Phe Asp Glu
                1040                1045                1050

tta ttt ctt atg aaa  cga gga gga caa gag  ata tac gtc ggt cca       3327
Leu Phe Leu Met Lys  Arg Gly Gly Gln Glu  Ile Tyr Val Gly Pro
                1055                1060                1065

tta ggt cgt gag tca  agc cat ttg ata aag  tat ttt gag tct ata       3372
Leu Gly Arg Glu Ser  Ser His Leu Ile Lys  Tyr Phe Glu Ser Ile
                1070                1075                1080

ccc ggt gta acc aaa  ata aag gag ggg tac  aat cca gca act tgg       3417
Pro Gly Val Thr Lys  Ile Lys Glu Gly Tyr  Asn Pro Ala Thr Trp
                1085                1090                1095

atg tta gaa gtc aca  tct tcg tct caa gaa  ata aca tta ggt gtt       3462
Met Leu Glu Val Thr  Ser Ser Ser Gln Glu  Ile Thr Leu Gly Val
                1100                1105                1110

gat ttt acc gaa tta  tac aag aac tca gac  ctc ttc cgg agg aac       3507
Asp Phe Thr Glu Leu  Tyr Lys Asn Ser Asp  Leu Phe Arg Arg Asn
                1115                1120                1125

aaa gct ttg atc gag  gaa cta agt gtg cca  cgc cct ggt aca agt       3552
Lys Ala Leu Ile Glu  Glu Leu Ser Val Pro  Arg Pro Gly Thr Ser
                1130                1135                1140

gac ctg cat ttt gaa  act gaa ttc tca cag  cca ttt tgg gtc caa       3597
Asp Leu His Phe Glu  Thr Glu Phe Ser Gln  Pro Phe Trp Val Gln
                1145                1150                1155

tgt atg gct tgt ttg  tgg aag caa cac tgg  tca tac tgg cgt aat       3642
Cys Met Ala Cys Leu  Trp Lys Gln His Trp  Ser Tyr Trp Arg Asn
                1160                1165                1170

ccg gct tat act gca  gtc aga ttt ctc ttc  aca acc ttc ata gct       3687
Pro Ala Tyr Thr Ala  Val Arg Phe Leu Phe  Thr Thr Phe Ile Ala
                1175                1180                1185

ctc ata ttc ggg tca  atg ttc tgg gat att  ggt aca aaa gtg agt       3732
Leu Ile Phe Gly Ser  Met Phe Trp Asp Ile  Gly Thr Lys Val Ser
                1190                1195                1200
```

```
ggg ccc caa gat ctg  aaa aac gcc atg gga  tct atg tat gct gct       3777
Gly Pro Gln Asp Leu  Lys Asn Ala Met Gly  Ser Met Tyr Ala Ala
                1205                 1210                 1215

gtc ctc ttc ctt ggt  gtg cag aat tca tcg  tca gtt cag ccc gtt       3822
Val Leu Phe Leu Gly  Val Gln Asn Ser Ser  Ser Val Gln Pro Val
                1220                 1225                 1230

gta tct gtc gaa cgt  act gta ttt tac aga  gaa aaa gct gct gga       3867
Val Ser Val Glu Arg  Thr Val Phe Tyr Arg  Glu Lys Ala Ala Gly
                1235                 1240                 1245

atg tac tcc gcg atg  ccc tat gcc ttt gca  caa gtt ttc atc gaa       3912
Met Tyr Ser Ala Met  Pro Tyr Ala Phe Ala  Gln Val Phe Ile Glu
                1250                 1255                 1260

att cct tat gta ttt  gta caa gct gtt gtc  tat ggt ctc att gtc       3957
Ile Pro Tyr Val Phe  Val Gln Ala Val Val  Tyr Gly Leu Ile Val
                1265                 1270                 1275

tat tct atg att gga  ttt gaa tgg act gct  gca aaa ttc ttt tgg       4002
Tyr Ser Met Ile Gly  Phe Glu Trp Thr Ala  Ala Lys Phe Phe Trp
                1280                 1285                 1290

tac ttc ttc ttc atg  ttc ttc acc ttc ctc  tac ttc acc ttc ttt       4047
Tyr Phe Phe Phe Met  Phe Phe Thr Phe Leu  Tyr Phe Thr Phe Phe
                1295                 1300                 1305

ggc atg atg acc gtg  gct gtt acc ccg aac  caa aat gtt gct tca       4092
Gly Met Met Thr Val  Ala Val Thr Pro Asn  Gln Asn Val Ala Ser
                1310                 1315                 1320

atc gtt gcc gga ttc  ttc tat aca gta tgg  aat ctc ttc tca gga       4137
Ile Val Ala Gly Phe  Phe Tyr Thr Val Trp  Asn Leu Phe Ser Gly
                1325                 1330                 1335

ttc atc gtt cca cga  cct cgt att ccg ata  tgg tgg aga tgg tac       4182
Phe Ile Val Pro Arg  Pro Arg Ile Pro Ile  Trp Trp Arg Trp Tyr
                1340                 1345                 1350

tac tgg gct tgc cct  gtt gca tgg aca ttg  tat ggt ttg gtt gca       4227
Tyr Trp Ala Cys Pro  Val Ala Trp Thr Leu  Tyr Gly Leu Val Ala
                1355                 1360                 1365

tct caa ttt gga gac  ctc caa gat aca att  aat gat caa act gtg       4272
Ser Gln Phe Gly Asp  Leu Gln Asp Thr Ile  Asn Asp Gln Thr Val
                1370                 1375                 1380

gaa gat ttc ttg aga  agt agc tat gga ttt  aag cat gat ttt cta       4317
Glu Asp Phe Leu Arg  Ser Ser Tyr Gly Phe  Lys His Asp Phe Leu
                1385                 1390                 1395

gga gtt gtt gca gct  gtg atc gtt gca ttt  gca gtt gtt ttc gcc       4362
Gly Val Val Ala Ala  Val Ile Val Ala Phe  Ala Val Val Phe Ala
                1400                 1405                 1410
```

```
ttc aca ttt gct ttg  ggt atc aag gca ttc  aat ttc cag aga aga       4407
Phe Thr Phe Ala Leu  Gly Ile Lys Ala Phe  Asn Phe Gln Arg Arg
                1415                1420                1425

tagaaatagt atttatttgt attcccagtt gttcatatat tcttgaataa gcttatgaag   4467

ttttaagtta ctgaatatgt tatgtcttac taatctttct caattcccag ttttgttgta   4527

taataacatg taataattgt tattcaaaaa aaaaaaaaaa aaaa                    4571
```

<210> 2
<211> 1425
<212> PRT
<213> Hyoscyamus muticus

<400> 2

```
Met Glu Pro Ser Asp Leu Ser Asn Phe Arg Gly Arg Ser Met Arg Gly
1               5                   10                  15

Ser Met Arg Gly Ser Val Arg Glu Asn Ser Asn Ser Ile Trp Arg Asn
            20                  25                  30

Asn Gly Val Glu Ile Phe Ser Arg Ser Thr Arg Asp Glu Asp Asp Glu
        35                  40                  45

Glu Ala Leu Lys Trp Ala Ala Leu Glu Lys Leu Pro Thr Tyr Asp Arg
    50                  55                  60

Leu Arg Lys Gly Ile Leu Phe Gly Ser Gln Gly Thr Gly Val Ala Glu
65                  70                  75                  80

Val Asp Val Asp Asp Leu Gly Val Gln Gln Arg Lys Asn Leu Leu Asp
                85                  90                  95

Arg Leu Val Lys Ile Ala Glu Glu Asp Asn Glu Lys Phe Leu Leu Lys
            100                 105                 110

Leu Lys Asn Arg Ile Asp Arg Val Gly Ile Asp Phe Pro Ser Ile Glu
        115                 120                 125

Val Arg Phe Glu His Leu Asn Ile Glu Ala Asp Ala Tyr Val Gly Ser
    130                 135                 140

Arg Ala Leu Pro Thr Phe Thr Asn Phe Ile Ser Asn Phe Ile Glu Ser
145                 150                 155                 160
```

Leu Leu Asp Ser Leu His Ile Leu Pro Ser Lys Lys Arg Ser Val Thr
165 170 175

Ile Leu Lys Asp Val Ser Gly Ile Val Lys Pro Cys Arg Met Thr Leu
180 185 190

Leu Leu Gly Pro Pro Gly Ser Gly Lys Thr Thr Leu Leu Leu Ala Leu
195 200 205

Ala Gly Lys Leu Asp Ser Ala Leu Arg Val Thr Gly Lys Val Thr Tyr
210 215 220

Asn Gly His Glu Leu His Glu Phe Val Pro Gln Arg Thr Ala Ala Tyr
225 230 235 240

Ile Ser Gln His Asp Leu His Ile Gly Glu Met Thr Val Arg Glu Thr
245 250 255

Leu Glu Phe Ser Ala Arg Cys Gln Gly Val Gly Ser Arg Tyr Glu Met
260 265 270

Leu Ala Glu Leu Ser Arg Arg Glu Lys Ala Ala Asn Ile Lys Pro Asp
275 280 285

Ala Asp Ile Asp Met Phe Met Lys Ala Ala Ser Thr Glu Gly Gln Glu
290 295 300

Ala Lys Val Ile Thr Asp Tyr Val Leu Lys Ile Leu Gly Leu Asp Ile
305 310 315 320

Cys Ala Asp Thr Met Val Gly Asp Gln Met Ile Arg Gly Ile Ser Gly
325 330 335

Gly Gln Lys Lys Arg Val Thr Thr Gly Glu Met Ile Val Gly Pro Ser
340 345 350

Lys Ala Leu Phe Met Asp Glu Ile Ser Thr Gly Leu Asp Ser Ser Thr
355 360 365

Thr Tyr Ser Ile Val Asn Ser Leu Lys Gln Ser Val Gln Ile Leu Lys
370 375 380

```
Gly Thr Ala Leu Ile Ser Leu Leu Gln Pro Ala Pro Glu Thr Tyr Asn
385                 390                 395                 400

Leu Phe Asp Asp Ile Val Leu Leu Ser Asp Gly Tyr Ile Val Tyr Gln
                405                 410                 415

Gly Pro Arg Glu Glu Val Leu Asp Phe Phe Glu Ser Met Gly Phe Lys
            420                 425                 430

Cys Pro Asn Arg Lys Gly Val Ala Asp Phe Leu Gln Glu Val Thr Ser
        435                 440                 445

Lys Lys Asp Gln Gln Gln Tyr Trp Val Lys Arg Asp Glu Pro Tyr Arg
    450                 455                 460

Phe Ile Thr Ser Lys Glu Phe Ala Glu Ala Tyr Gln Ser Phe His Val
465                 470                 475                 480

Gly Arg Lys Val Ser Asp Glu Leu Thr Thr Ala Phe Asp Lys Ser Lys
                485                 490                 495

Ser His Pro Ala Ala Leu Thr Thr Glu Lys Tyr Gly Ile Gly Val Lys
            500                 505                 510

Gln Leu Leu Lys Val Cys Thr Glu Arg Glu Phe Leu Leu Met Gln Arg
        515                 520                 525

Asn Ser Phe Val Tyr Ile Phe Lys Phe Phe Gln Leu Met Val Ile Ala
    530                 535                 540

Leu Met Thr Met Thr Ile Phe Phe Arg Thr Lys Met Ser Arg Asp Thr
545                 550                 555                 560

Glu Thr Asp Gly Gly Ile Tyr Ser Gly Ala Leu Phe Phe Thr Val Val
                565                 570                 575

Met Leu Met Phe Asn Gly Leu Ser Glu Leu Pro Leu Thr Leu Tyr Lys
            580                 585                 590

Leu Pro Val Phe Tyr Lys Gln Arg Asp Phe Leu Phe Tyr Pro Ser Trp
        595                 600                 605
```

Ala Tyr Ala Val Pro Ser Trp Ile Leu Lys Ile Pro Val Thr Phe Leu
610 615 620

Glu Val Gly Met Trp Val Phe Leu Thr Tyr Tyr Val Ile Gly Phe Asp
625 630 635 640

Pro Asn Val Gly Arg Phe Phe Lys Gln Phe Leu Leu Leu Ile Val Val
645 650 655

Asn Gln Met Ala Ser Gly Leu Phe Arg Phe Ile Ala Ala Val Gly Arg
660 665 670

Thr Met Gly Val Ala Ser Thr Phe Gly Ala Phe Ala Leu Leu Leu Gln
675 680 685

Phe Ala Leu Gly Gly Phe Val Leu Ala Arg Thr Asp Val Lys Asp Trp
690 695 700

Trp Ile Trp Gly Tyr Trp Thr Ser Pro Leu Met Phe Ser Val Asn Ala
705 710 715 720

Ile Leu Val Asn Glu Phe Asp Gly Lys Lys Trp Lys His Ile Ala Pro
725 730 735

Asn Gly Thr Glu Pro Leu Gly Pro Ala Val Val Arg Ser Gln Gly Phe
740 745 750

Phe Pro Asp Ala Tyr Trp Tyr Trp Ile Gly Val Gly Ala Leu Val Gly
755 760 765

Phe Thr Val Leu Phe Asn Ile Ala Tyr Ser Leu Ala Leu Ala Tyr Leu
770 775 780

Asn Pro Phe Gly Lys Pro Gln Ala Thr Ile Ser Glu Glu Ser Glu Ser
785 790 795 800

Asn Glu Asn Ser Glu Leu Ser Thr Pro Ile Ala Ser Thr Thr Glu Gly
805 810 815

Asp Ser Val Gly Glu Asn Gln Asn Lys Lys Gly Met Val Leu Pro Phe
820 825 830

Glu Pro His Ser Ile Thr Phe Asp Glu Val Val Tyr Ser Val Asp Met
835 840 845

Pro Pro Glu Met Arg Glu Gln Gly Thr Ser Asp Asn Arg Leu Val Leu
850 855 860

Leu Lys Ser Val Ser Gly Ala Phe Arg Pro Gly Val Leu Thr Ala Leu
865 870 875 880

Met Gly Val Ser Gly Ala Gly Lys Thr Thr Leu Met Asp Val Leu Ala
885 890 895

Gly Arg Lys Thr Gly Gly Tyr Ile Asp Gly Ser Ile Asn Ile Ser Gly
900 905 910

Tyr Pro Lys Lys Gln Glu Thr Phe Ala Arg Ile Ser Gly Tyr Cys Glu
915 920 925

Gln Asn Asp Ile His Ser Pro Tyr Val Thr Val Tyr Glu Ser Leu Val
930 935 940

Tyr Ser Ala Trp Leu Arg Leu Pro Gln Asp Val Asp Glu Lys Lys Arg
945 950 955 960

Met Met Phe Val Glu Gln Val Met Glu Leu Val Glu Leu Thr Pro Leu
965 970 975

Arg Ser Ala Leu Val Gly Leu Pro Gly Val Asn Gly Leu Thr Ile Ala
980 985 990

Val Glu Leu Val Ala Asn Pro Ser Ile Ile Phe Met Asp Glu Pro Thr
995 1000 1005

Ser Gly Leu Asp Ala Arg Ala Ala Ala Ile Val Met Arg Ala Val
1010 1015 1020

Arg Asn Thr Val Asp Thr Gly Arg Thr Val Val Cys Thr Ile His
1025 1030 1035

Gln Pro Ser Ile Asp Ile Phe Glu Ala Phe Asp Glu Leu Phe Leu
1040 1045 1050

Met Lys Arg Gly Gly Gln Glu Ile Tyr Val Gly Pro Leu Gly Arg
1055 1060 1065

Glu Ser Ser His Leu Ile Lys Tyr Phe Glu Ser Ile Pro Gly Val
1070 1075 1080

Thr Lys Ile Lys Glu Gly Tyr Asn Pro Ala Thr Trp Met Leu Glu
1085 1090 1095

Val Thr Ser Ser Ser Gln Glu Ile Thr Leu Gly Val Asp Phe Thr
1100 1105 1110

Glu Leu Tyr Lys Asn Ser Asp Leu Phe Arg Arg Asn Lys Ala Leu
1115 1120 1125

Ile Glu Glu Leu Ser Val Pro Arg Pro Gly Thr Ser Asp Leu His
1130 1135 1140

Phe Glu Thr Glu Phe Ser Gln Pro Phe Trp Val Gln Cys Met Ala
1145 1150 1155

Cys Leu Trp Lys Gln His Trp Ser Tyr Trp Arg Asn Pro Ala Tyr
1160 1165 1170

Thr Ala Val Arg Phe Leu Phe Thr Thr Phe Ile Ala Leu Ile Phe
1175 1180 1185

Gly Ser Met Phe Trp Asp Ile Gly Thr Lys Val Ser Gly Pro Gln
1190 1195 1200

Asp Leu Lys Asn Ala Met Gly Ser Met Tyr Ala Ala Val Leu Phe
1205 1210 1215

Leu Gly Val Gln Asn Ser Ser Ser Val Gln Pro Val Val Ser Val
1220 1225 1230

Glu Arg Thr Val Phe Tyr Arg Glu Lys Ala Ala Gly Met Tyr Ser
1235 1240 1245

Ala Met Pro Tyr Ala Phe Ala Gln Val Phe Ile Glu Ile Pro Tyr
1250 1255 1260

Val Phe Val Gln Ala Val Val Tyr Gly Leu Ile Val Tyr Ser Met
1265 1270 1275

Ile Gly Phe Glu Trp Thr Ala Ala Lys Phe Phe Trp Tyr Phe Phe
1280 1285 1290

Phe Met Phe Phe Thr Phe Leu Tyr Phe Thr Phe Phe Gly Met Met
1295 1300 1305

Thr Val Ala Val Thr Pro Asn Gln Asn Val Ala Ser Ile Val Ala
1310 1315 1320

Gly Phe Phe Tyr Thr Val Trp Asn Leu Phe Ser Gly Phe Ile Val
1325 1330 1335

Pro Arg Pro Arg Ile Pro Ile Trp Trp Arg Trp Tyr Tyr Trp Ala
1340 1345 1350

Cys Pro Val Ala Trp Thr Leu Tyr Gly Leu Val Ala Ser Gln Phe
1355 1360 1365

Gly Asp Leu Gln Asp Thr Ile Asn Asp Gln Thr Val Glu Asp Phe
1370 1375 1380

Leu Arg Ser Ser Tyr Gly Phe Lys His Asp Phe Leu Gly Val Val
1385 1390 1395

Ala Ala Val Ile Val Ala Phe Ala Val Val Phe Ala Phe Thr Phe
1400 1405 1410

Ala Leu Gly Ile Lys Ala Phe Asn Phe Gln Arg Arg
1415 1420 1425

<210> 3
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer in example 3.1

<400> 3
aaaaagcagg ctaccatgcc cgaggccaag cttaacaata 40

<210> 4

<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer of example 3.1

<400> 4
agaaagctgg gtccatcttg gtaagtttct tttcttaacc 40

<210> 5
<211> 37
<212> PRT
<213> Ipomoea batatas

<300>
<301> Matsuoka and Nakamura
<302> Propeptide of a precursor to a plant vacuolar protein required for vacuolar targeting
<303> Proc. Natl. Acad. Sci. USA
<304> 88
<305> 3
<306> 834-8
<307> 1991-02-01
<308> PMID: 1992474
<309> 1991-02-01
<313> (1)..(37)

<400> 5

Met Lys Ala Phe Thr Leu Ala Leu Phe Leu Ala Leu Ser Leu Tyr Leu
1 5 10 15

Leu Pro Asn Pro Ala His Ser Arg Phe Asn Pro Ile Arg Leu Pro Thr
20 25 30

Thr His Glu Pro Ala
35

<210> 6
<211> 12
<212> PRT
<213> Nicotiana tabacum

<300>
<301> Neuhaus, J.M.; Sticher, L.; Meins, F. and Boller, T.
<302> A short C-terminal sequence is necessary and sufficient for the targeting of chitinases to the plant vacuole
<303> Proc. Natl. Acad. Sci. USA
<304> 88
<305> 22
<306> 10362-10366
<307> 1991-11-15

<308> PMID: 1946457
<309> 1991-11-25
<313> (318)..(329)

<400> 6

Asp Leu Leu Gly Asn Gly Leu Leu Val Asp Thr Met
1 5 10

<210> 7
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer in example 5.1

<400> 7
aaaaagcagg ctaccatgga gacgttatcg agaa 34

<210> 8
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer in example 5.1

<400> 8
agaaagctgg gtctatcgtt gttggaagtt gagc 34

<210> 9
<211> 12789
<212> DNA
<213> Artificial Sequence

<220>
<223> vector pK7WG2D

<220>
<221> misc_feature
<222> (4772)..(4772)
<223> n can be any base

<400> 9
tgatcacagg cagcaacgct ctgtcatcgt tacaatcaac atgctaccct ccgcgagatc 60

atccgtgttt caaacccggc agcttagttg ccgttcttcc gaatagcatc ggtaacatga 120

gcaaagtctg ccgccttaca acggctctcc cgctgacgcc gtcccggact gatgggctgc 180

ctgtatcgag tggtgatttt gtgccgagct gccggtcggg gagctgttgg ctggctggtg 240

gcaggatata ttgtggtgta aacaaattga cgcttagaca acttaataac acattgcgga 300

cgtttttaat gtactgaatt aacgccgaat tgaattatca gcttgcatgc cggtcgatct 360

agtaacatag atgacaccgc gcgcgataat ttatcctagt ttgcgcgcta tattttgttt 420

tctatcgcgt attaaatgta taattgcggg actctaatca aaaaacccat ctcataaata 480

acgtcatgca ttacatgtta attattacat gcttaacgta attcaacaga aattatatga 540

taatcatcgc aagaccggca acaggattca atcttaagaa actttattgc caaatgtttg 600

aacgatctgc ttgactctag ctagagtccg aaccccagag tcccgctcag aagaactcgt 660

caagaaggcg atagaaggcg atgcgctgcg aatcgggagc ggcgataccg taaagcacga 720

ggaagcggtc agcccattcg ccgccaagct cttcagcaat atcacgggta gccaacgcta 780

tgtcctgata gcggtccgcc acacccagcc ggccacagtc gatgaatcca gaaaagcggc 840

cattttccac catgatattc ggcaagcagg catcgccctg ggtcacgacg agatcctcgc 900

cgtcgggcat ccgcgccttg agcctggcga acagttcggc tggcgcgagc ccctgatgct 960

cttcgtccag atcatcctga tcgacaagac cggcttccat ccgagtacgt cctcgctcga 1020

tgcgatgttt cgcttggtgg tcgaatgggc aggtagccgg atcaagcgta tgcagccgcc 1080

gcattgcatc agccatgatg gatactttct cggcaggagc aaggtgagat gacaggagat 1140

cctgccccgg cacttcgccc aatagcagcc agtcccttcc cgcttcagtg acaacgtcga 1200

gcacagctgc gcaaggaacg cccgtcgtgg ccagccacga tagccgcgct gcctcgtctt 1260

ggagttcatt cagggcaccg gacaggtcgg tcttgacaaa aagaaccggg cgcccctgcg 1320

ctgacagccg gaacacggcg gcatcagagc agccgattgt ctgttgtgcc cagtcatagc 1380

cgaatagcct ctccacccaa gcggccggag aacctgcgtg caatccatct tgttcaatca 1440

tgcctcgatc gagttgagag tgaatatgag actctaattg gataccgagg ggaatttatg 1500

gaacgtcagt ggagcatttt tgacaagaaa tatttgctag ctgatagtga ccttaggcga 1560

cttttgaacg cgcaataatg gtttctgacg tatgtgctta gctcattaaa ctccagaaac 1620

ccgcggctga gtggctcctt caacgttgcg gttctgtcag ttccaaacgt aaaacggctt 1680

gtcccgcgtc atcggcgggg gtcataacgt gactccctta attctcatgt atgataattc 1740

gcggtacccg gggatcctct agagggcccg acgtcgcatg cctgcaggtc actggatttt 1800

ggttttagga attagaaatt ttattgatag aagtatttta caaatacaaa tacatactaa 1860

gggtttctta tatgctcaac acatgagcga aaccctataa gaaccctaat tcccttatct 1920

gggaactact cacacattat tctggagaaa aatagagaga gatagatttg tagagagaga 1980

ctggtgattt ttgcggactc tagcatggcc gcgggatatc accactttgt acaagaaagc 2040

tgaacgagaa acgtaaaatg atataaatat caatatatta aattagattt tgcataaaaa 2100

acagactaca taatactgta aaacacaaca tatccagtca ctatggtcga cctgcagact 2160

ggctgtgtat aagggagcct gacatttata ttccccagaa catcaggtta atggcgtttt 2220

tgatgtcatt ttcgcggtgg ctgagatcag ccacttcttc cccgataacg gagaccggca 2280

cactggccat atcggtggtc atcatgcgcc agctttcatc cccgatatgc accaccgggt 2340

aaagttcacg ggagacttta tctgacagca gacgtgcact ggccaggggg atcaccatcc 2400

gtcgcccggg cgtgtcaata atatcactct gtacatccac aaacagacga taacggctct 2460

ctcttttata ggtgtaaacc ttaaactgca tttcaccagt ccctgttctc gtcagcaaaa 2520

gagccgttca tttcaataaa ccgggcgacc tcagccatcc cttcctgatt ttccgctttc 2580

cagcgttcgg cacgcagacg acgggcttca ttctgcatgg ttgtgcttac cagaccggag 2640

atattgacat catatatgcc ttgagcaact gatagctgtc gctgtcaact gtcactgtaa 2700

tacgctgctt catagcacac ctctttttga catacttcgg gtatacatat cagtatatat 2760

tcttataccg caaaaatcag cgcgcaaata cgcatactgt tatctggctt ttagtaagcc 2820

ggatccacgc gtttacgccc cgccctgcca ctcatcgcag tactgttgta attcattaag 2880

cattctgccg acatggaagc catcacagac ggcatgatga acctgaatcg ccagcggcat 2940

cagcaccttg tcgccttgcg tataatattt gcccatggtg aaaacggggg cgaagaagtt 3000

gtccatattg gccacgttta aatcaaaact ggtgaaactc acccagggat tggctgagac 3060

gaaaaacata ttctcaataa acccttttagg gaaataggcc aggttttcac cgtaacacgc 3120

cacatcttgc gaatatatgt gtagaaactg ccggaaatcg tcgtggtatt cactccagag 3180

cgatgaaaac gtttcagttt gctcatggaa aacggtgtaa caagggtgaa cactatccca 3240

tatcaccagc tcaccgtctt tcattgccat acggaattcc ggatgagcat tcatcaggcg 3300

ggcaagaatg tgaataaagg ccggataaaa cttgtgctta tttttcttta cggtctttaa 3360

aaaggccgta atatccagct gaacggtctg gttataggta cattgagcaa ctgactgaaa 3420

tgcctcaaaa tgttctttac gatgccattg ggatatatca acggtggtat atccagtgat 3480

ttttttctcc attttagctt ccttagctcc tgaaaatctc gccggatcct aactcaaaat 3540

ccacacatta tacgagccgg aagcataaag tgtaaagcct ggggtgccta atgcggccgc 3600

catagtgact ggatatgttg tgttttacag tattatgtag tctgtttttt atgcaaaatc 3660

taatttaata tattgatatt tatatcattt tacgtttctc gttcagcttt tttgtacaaa 3720

cttgtgatat cactagtgcg gccgcctgca ggtcgactag aatagtaaat tgtaatgttg 3780

tttgttgttt gttttgttgt ggtaattgtt gtaaaaatac ggatcgtcct gcagtcctct 3840

ccaaatgaaa tgaacttcct tatatagagg aagggtcttg cgaaggatag tgggattgtg 3900

cgtcatccct tacgtcagtg gagatatcac atcaatccac ttgctttgaa gacgtggttg 3960

gaacgtcttc tttttccacg atgctcctcg tgggtggggg tccatctttg ggaccactgt 4020

cggcagaggc atcttgaacg atagcctttc ctttatcgca atgatggcat ttgtaggtgc 4080

caccttcctt ttctactgtc cttttgatga agtgacagat agctgggcaa tggaatccga 4140

ggaggtttcc cgatattacc ctttgttgaa aagtctcaat agccctttgg tcttctgaga 4200

ctgtatcttt gatattcttg gagtagacga gagtgtcgtg ctccaccatg ttgacgaaga 4260

ttttcttctt gtcattgagt cgtaaaagac tctgtatgaa ctgttcgcca gtcttcacgg 4320

cgagttctgt tagatcctcg atctgaattt ttgactccat ggcctttgat tcagtaggaa 4380

ctactttctt agagactcca atctctatta cttgccttgg tttatgaagc aagccttgaa 4440

tcgtccatac tggaatagta cttctgatct tgagaaatat atctttctct gtgttcttga 4500

tgcagttagt cctgaatctt ttgactgcat ctttaacctt cttgggaagg tatttgatct 4560

cctggagatt attactcggg tagatcgtct tgatgagacc tgccgcgtag gcctctctaa 4620

ccatctgtgg gtcagcattc tttctgaaat tgaagaggct aatcttctca ttatcggtgg 4680

tgaacatggt atcgtcacct tctccgtcga actttcttcc tagatcgtag agatagagaa 4740

agtcgtccat ggtgatctcc ggggcaaagg anatctcgac catatgggag agctcaagct 4800

tgcatgcctg caggtcactg gattttggtt ttaggaatta gaaattttat tgatagaagt 4860

attttacaaa tacaaataca tactaagggt ttcttatatg ctcaacacat gagcgaaacc 4920

ctataagaac cctaattccc ttatgtggga actactcaca cattattctg gagaaaaata 4980

gagagagata gatttgtaga gagagactgg tgatttttgc ggactctaga actagtggat 5040

cccccgggct gcagccgggc ggcgcttaca gctcgtcctt cttgtacagc tcgtccatgc 5100

cgagagtgat cccggcggcg gtcacgaact ccagcaggac catgtgatcg cgcttctcgt 5160

tggggtcttt gctcagggcg gactgggtgc tcaggtagtg gttgtcgggc agcagcacgg 5220

ggccgtcgcc gatgggggtg ttctgctggt agtggtcggc gagctgcacg ctgccgtcct 5280

cgatgttgtg gcggatcttg aagttcacct tgatgccgtt cttctgcttg tcggccatga 5340

tatagacgtt gtggctgttg tagttgtact ccagcttgtg ccccaggatg ttgccgtcct 5400

ccttgaagtc gatgcccttc agctcgatgc ggttcaccag ggtgtcgccc tcgaacttca 5460

cctcggcgcg ggtcttgtag ttgccgtcgt ccttgaagaa gatggtgcgc tcctggacgt 5520

agccttcggg catggcggac ttgaagaagt cgtgctgctt catgtggtcg gggtagcggc 5580

tgaagcactg cacgccgtag gtcagggtgg tcacgagggt gggccagggc acgggcagct 5640

tgccggtggt gcagatgaac ttcagggtca gcttgccgta ggtggcatcg ccctcgccct 5700

cgccggacac gctgaacttg tggccgttta cgtcgccgtc cagctcgacc aggatgggca 5760

ccaccccggt gaacagctcc tcgcccttgc tcaccatgtc ggccgaggat aatgatagga 5820

gaagtgaaaa gatgaaaaag agaaaaagat tagtcttcac catggctatc gttcgtaaat 5880

ggtgaaaatt ttcagaaaat agcttttgct ttaaaagaaa tgatttaaat tgctgcaata 5940

gaagtagaat gcttgattgc ttgagattcg tttgttttgt atatgttgtg ttgagaattc 6000

gagctcggta cccggggatc ctctagcgaa ttttctctgc tcaaattgtt gaggttagcg 6060

gatttgtaaa cgcgtttata tgggctgctt ggagggtact tttggattaa ttttttttctg 6120

ccagcgcatt ctgacgcggc accgctttgg aaagtgcgct gtgggtccgc gttttctaca 6180

ataatgtgcc gatccggtca gaaagtatat ggatgagttg tgccagcctc accaacgtgc 6240

tgcaggccca tcatgactac ttcaatgtta atgggggtaa tgaataaata ggcgaaattg 6300

ggttcacggt gggcccaggg aatataatat tgccgcagag gtagtcggat gccaaggccc 6360

gcaactaata gttcacgaac aaattcctag agagtcgacc tgcagcatgc aagctaacct 6420

gcaggcatgc aagcttagct tgagcttgga tcagattgtc gtttcccgcc ttcagtttaa 6480

actatcagtg tttgacagga tatattggcg ggtaaaccta agagaaaaga gcgtttatta 6540

gaataacgga tatttaaaag ggcgtgaaaa ggtttatccg ttcgtccatt tgtatgtgca 6600

tgccaaccac agggttcccc tcgggatcaa agtactttga tccaacccct ccgctgctat 6660

agtgcagtcg gcttctgacg ttcagtgcag ccgtcttctg aaaacgacat gtcgcacaag 6720

tcctaagtta cgcgacaggc tgccgccctg ccctttttcct ggcgttttct tgtcgcgtgt 6780

tttagtcgca taaagtagaa tacttgcgac tagaaccgga gacattacgc catgaacaag 6840

agcgccgccg ctggcctgct gggctatgcc cgcgtcagca ccgacgacca ggacttgacc 6900

aaccaacggg ccgaactgca cgcggccggc tgcaccaagc tgttttccga gaagatcacc 6960

ggcaccaggc gcgaccgccc ggagctggcc aggatgcttg accacctacg ccctggcgac 7020

gttgtgacag tgaccaggct agaccgcctg gcccgcagca cccgcgacct actggacatt 7080

gccgagcgca tccaggaggc cggcgcgggc ctgcgtagcc tggcagagcc gtgggccgac 7140

accaccacgc cggccggccg catggtgttg accgtgttcg ccggcattgc cgagttcgag 7200

cgttccctaa tcatcgaccg cacccggagc gggcgcgagg ccgccaaggc ccgaggcgtg 7260

aagtttggcc cccgccctac cctcaccccg gcacagatcg cgcacgcccg cgagctgatc 7320

gaccaggaag gccgcaccgt gaaagaggcg gctgcactgc ttggcgtgca tcgctcgacc 7380

ctgtaccgcg cacttgagcg cagcgaggaa gtgacgccca ccgaggccag gcggcgcggt 7440

gccttccgtg aggacgcatt gaccgaggcc gacgccctgg cggccgccga gaatgaacgc 7500

caagaggaac aagcatgaaa ccgcaccagg acggccagga cgaaccgttt ttcattaccg 7560

aagagatcga ggcggagatg atcgcggccg ggtacgtgtt cgagccgccc gcgcacgtct 7620

caaccgtgcg gctgcatgaa atcctggccg gtttgtctga tgccaagctg gcggcctggc 7680

cggccagctt ggccgctgaa gaaaccgagc gccgccgtct aaaaaggtga tgtgtatttg 7740

agtaaaacag cttgcgtcat gcggtcgctg cgtatatgat gcgatgagta aataaacaaa 7800

tacgcaaggg gaacgcatga aggttatcgc tgtacttaac cagaaaggcg ggtcaggcaa 7860

gacgaccatc gcaacccatc tagcccgcgc cctgcaactc gccggggccg atgttctgtt 7920

agtcgattcc gatccccagg gcagtgcccg cgattgggcg gccgtgcggg aagatcaacc 7980

gctaaccgtt gtcggcatcg accgcccgac gattgaccgc gacgtgaagg ccatcggccg 8040

gcgcgacttc gtagtgatcg acggagcgcc ccaggcggcg gacttggctg tgtccgcgat 8100

caaggcagcc gacttcgtgc tgattccggt gcagccaagc ccttacgaca tatgggccac 8160

cgccgacctg gtggagctgg ttaagcagcg cattgaggtc acggatggaa ggctacaagc 8220

ggcctttgtc gtgtcgcggg cgatcaaagg cacgcgcatc ggcggtgagg ttgccgaggc 8280

gctggccggg tacgagctgc ccattcttga gtcccgtatc acgcagcgcg tgagctaccc 8340

aggcactgcc gccgccggca caaccgttct tgaatcagaa cccgagggcg acgctgcccg 8400

cgaggtccag gcgctggccg ctgaaattaa atcaaaactc atttgagtta atgaggtaaa 8460

gagaaaatga gcaaaagcac aaacacgcta agtgccggcc gtccgagcgc acgcagcagc 8520

aaggctgcaa cgttggccag cctggcagac acgccagcca tgaagcgggt caactttcag 8580

ttgccggcgg aggatcacac caagctgaag atgtacgcgg tacgccaagg caagaccatt 8640

accgagctgc tatctgaata catcgcgcag ctaccagagt aaatgagcaa atgaataaat 8700

gagtagatga attttagcgg ctaaaggagg cggcatggaa aatcaagaac aaccaggcac 8760

cgacgccgtg gaatgcccca tgtgtggagg aacgggcggt tggccaggcg taagcggctg 8820

ggttgtctgc cggccctgca atggcactgg aacccccaag cccgaggaat cggcgtgacg 8880

gtcgcaaacc atccggcccg gtacaaatcg gcgcggcgct gggtgatgac ctggtggaga 8940

agttgaaggc cgcgcaggcc gcccagcggc aacgcatcga ggcagaagca cgccccggtg 9000

aatcgtggca agcggccgct gatcgaatcc gcaaagaatc ccggcaaccg ccggcagccg 9060

gtgcgccgtc gattaggaag ccgcccaagg gcgacgagca accagatttt ttcgttccga 9120

tgctctatga cgtgggcacc cgcgatagtc gcagcatcat ggacgtggcc gttttccgtc 9180

tgtcgaagcg tgaccgacga gctggcgagg tgatccgcta cgagcttcca gacgggcacg 9240

tagaggtttc cgcagggccg gccggcatgg ccagtgtgtg ggattacgac ctggtactga 9300

tggcggtttc ccatctaacc gaatccatga accgataccg ggaagggaag ggagacaagc 9360

ccggccgcgt gttccgtcca cacgttgcgg acgtactcaa gttctgccgg cgagccgatg 9420

gcggaaagca gaaagacgac ctggtagaaa cctgcattcg gttaaacacc acgcacgttg 9480

ccatgcagcg tacgaagaag gccaagaacg gccgcctggt gacggtatcc gagggtgaag 9540

ccttgattag ccgctacaag atcgtaaaga gcgaaaccgg gcggccggag tacatcgaga 9600

tcgagctagc tgattggatg taccgcgaga tcacagaagg caagaacccg gacgtgctga 9660

cggttcaccc cgattacttt ttgatcgatc ccggcatcgg ccgttttctc taccgcctgg 9720

cacgccgcgc cgcaggcaag gcagaagcca gatggttgtt caagacgatc tacgaacgca 9780

gtggcagcgc cggagagttc aagaagttct gtttcaccgt gcgcaagctg atcgggtcaa 9840

atgacctgcc ggagtacgat ttgaaggagg aggcggggca ggctggcccg atcctagtca 9900

tgcgctaccg caacctgatc gagggcgaag catccgccgg ttcctaatgt acggagcaga 9960

tgctagggca aattgcccta gcaggggaaa aaggtcgaaa aggtctcttt cctgtggata 10020

gcacgtacat tgggaaccca aagccgtaca ttgggaaccg gaacccgtac attgggaacc 10080

caaagccgta cattgggaac cggtcacaca tgtaagtgac tgatataaaa gagaaaaaag 10140

gcgatttttc cgcctaaaac tctttaaaac ttattaaaac tcttaaaacc cgcctggcct 10200

gtgcataact gtctggccag cgcacagccg aagagctgca aaaagcgcct acccttcggt 10260

cgctgcgctc cctacgcccc gccgcttcgc gtcggcctat cgcggccgct ggccgctcaa 10320

aaatggctgg cctacggcca ggcaatctac cagggcgcgg acaagccgcg ccgtcgccac 10380

tcgaccgccg gcgcccacat caaggcaccc tgcctcgcgc gtttcggtga tgacggtgaa 10440

aacctctgac acatgcagct cccggagacg gtcacagctt gtctgtaagc ggatgccggg 10500

agcagacaag cccgtcaggg cgcgtcagcg ggtgttggcg ggtgtcgggg cgcagccatg 10560

acccagtcac gtagcgatag cggagtgtat actggcttaa ctatgcggca tcagagcaga 10620

ttgtactgag agtgcaccat atgcggtgtg aaataccgca cagatgcgta aggagaaaat 10680

accgcatcag gcgctcttcc gcttcctcgc tcactgactc gctgcgctcg gtcgttcggc 10740

tgcggcgagc ggtatcagct cactcaaagg cggtaatacg gttatccaca gaatcagggg 10800

ataacgcagg aaagaacatg tgagcaaaag gccagcaaaa ggccaggaac cgtaaaaagg 10860

ccgcgttgct ggcgtttttc cataggctcc gccccctga cgagcatcac aaaaatcgac 10920

gctcaagtca gaggtggcga aacccgacag gactataaag ataccaggcg tttccccctg 10980

gaagctccct cgtgcgctct cctgttccga ccctgccgct taccggatac ctgtccgcct 11040

ttctcccttc gggaagcgtg gcgctttctc atagctcacg ctgtaggtat ctcagttcgg 11100

tgtaggtcgt tcgctccaag ctgggctgtg tgcacgaacc ccccgttcag cccgaccgct 11160

gcgccttatc cggtaactat cgtcttgagt ccaacccggt aagacacgac ttatcgccac 11220

tggcagcagc cactggtaac aggattagca gagcgaggta tgtaggcggt gctacagagt 11280

tcttgaagtg gtggcctaac tacggctaca ctagaaggac agtatttggt atctgcgctc 11340

tgctgaagcc agttaccttc ggaaaaagag ttggtagctc ttgatccggc aaacaaacca 11400

ccgctggtag cggtggtttt tttgtttgca agcagcagat tacgcgcaga aaaaaaggat 11460

ctcaagaaga tcctttgatc ttttctacgg ggtctgacgc tcagtggaac gaaaactcac 11520

gttaagggat tttggtcatg catgatatat ctcccaattt gtgtagggct tattatgcac 11580

gcttaaaaat aataaaagca gacttgacct gatagtttgg ctgtgagcaa ttatgtgctt 11640

agtgcatcta atcgcttgag ttaacgccgg cgaagcggcg tcggcttgaa cgaatttcta 11700

gctagacatt atttgccgac taccttggtg atctcgcctt tcacgtagtg gacaaattct 11760

tccaactgat ctgcgcgcga ggccaagcga tcttcttctt gtccaagata agcctgtcta 11820

gcttcaagta tgacgggctg atactgggcc ggcaggcgct ccattgccca gtcggcagcg 11880

acatccttcg gcgcgatttt gccggttact gcgctgtacc aaatgcggga caacgtaagc 11940

actacatttc gctcatcgcc agcccagtcg ggcggcgagt tccatagcgt taaggtttca 12000

tttagcgcct caaatagatc ctgttcagga accggatcaa agagttcctc cgccgctgga 12060

cctaccaagg caacgctatg ttctcttgct tttgtcagca agatagccag atcaatgtcg 12120

atcgtggctg gctcgaagat acctgcaaga atgtcattgc gctgccattc tccaaattgc 12180

agttcgcgct tagctggata acgccacgga atgatgtcgt cgtgcacaac aatggtgact 12240

tctacagcgc ggagaatctc gctctctcca ggggaagccg aagtttccaa aaggtcgttg 12300

atcaaagctc gccgcgttgt ttcatcaagc cttacggtca ccgtaaccag caaatcaata 12360

tcactgtgtg gcttcaggcc gccatccact gcggagccgt acaaatgtac ggccagcaac 12420

gtcggttcga gatggcgctc gatgacgcca actacctctg atagttgagt cgatacttcg 12480

gcgatcaccg cttcccccat gatgtttaac tttgttttag ggcgactgcc ctgctgcgta 12540

acatcgttgc tgctccataa catcaaacat cgacccacgg cgtaacgcgc ttgctgcttg 12600

gatgcccgag gcatagactg taccccaaaa aaacatgtca taacaagaag ccatgaaaac 12660

cgccactgcg ccgttaccac cgctgcgttc ggtcaaggtt ctggaccagt tgcgtgacgg 12720

cagttacgct acttgcatta cagcttacga accgaacgag gcttatgtcc actgggttcg 12780

tgcccgaat 12789

<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate primer ALGG39

<220>
<221> misc_feature
<222> (3)..(3)
<223> Inosine

<220>
<221> misc_feature
<222> (9)..(9)
<223> Inosine

<220>
<221> misc_feature
<222> (11)..(11)
<223> Inosine

<220>
<221> misc_feature
<222> (15)..(15)
<223> g or a

<220>
<221> misc_feature
<222> (18)..(18)

<223> any base

<400> 10
ccargykcag gaaaracnac 20

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate primer ALGG40

<220>
<221> misc_feature
<222> (3)..(3)
<223> Inosine

<220>
<221> misc_feature
<222> (15)..(15)
<223> any base

<220>
<221> misc_feature
<222> (18)..(18)
<223> any base

<400> 11
acackyttyt tytgnccncc 20

<210> 12
<211> 8
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate primer ALGG41

<220>
<221> misc_feature
<222> (6)..(6)
<223> any base

<220>
<221> misc_feature
<222> (5)..(5)
<223> g or a

<220>
<221> misc_feature
<222> (3)..(3)
<223> any base

<400> 12
tcnarncc 8

<210> 13
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate primer ALGG42

<220>
<221> misc_feature
<222> (3)..(3)
<223> Inosine

<220>
<221> misc_feature
<222> (6)..(6)
<223> Inosine

<220>
<221> misc_feature
<222> (9)..(9)
<223> Inosine

<220>
<221> misc_feature
<222> (12)..(12)
<223> Inosine

<220>
<221> misc_feature
<222> (15)..(15)
<223> any base

<220>
<221> misc_feature
<222> (18)..(18)
<223> any base

<400> 13
ggagtaytaa cagcnytnat ggg 23

<210> 14
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate primer ALGG43

<220>
<221> misc_feature
<222> (3)..(3)
<223> any base

<220>
<221> misc_feature
<222> (18)..(18)
<223> any base

<220>
<221> misc_feature
<222> (5)..(5)
<223> g or a

<220>
<221> misc_feature
<222> (21)..(21)
<223> g or a

<220>
<221> misc_feature
<222> (12)..(12)
<223> Inosine

<220>
<221> misc_feature
<222> (15)..(15)
<223> Inosine

<400> 14
tcnarcatcc aagtagcngg rtt 23

<210> 15
<211> 8
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate primer ALGG44

<220>
<221> misc_feature
<222> (6)..(6)
<223> g or a

<400> 15
ckccarta 8